



#231600

RAW SEQUENCE LISTING

DATE: 01/28/2003

PATENT APPLICATION: US/09/585,645A

TIME: 16:20:49

Input Set : N:\vernette\09585645A.RAW.txt

Output Set: N:\CRF4\01282003\I585645A.raw

3 <110> APPLICANT: Zoghbi, Huda
4 Bellen, Hugo
5 Bermingham, Nessim
6 Hassan, Bessam
7 Ben-Arie, Nissim
9 <120> TITLE OF INVENTION: Compositions and Methods for Therapeutic Use of Atonal-associated Sequence
10 for Deafness, Osteoarthritis, and Abnormal Cell Proliferation
12 <130> FILE REFERENCE: P01899US2
14 <140> CURRENT APPLICATION NUMBER: US 09/585,645A
15 <141> CURRENT FILING DATE: 2000-06-01
17 <150> PRIOR APPLICATION NUMBER: US 60/137,060
18 <151> PRIOR FILING DATE: 1999-06-01
20 <150> PRIOR APPLICATION NUMBER: US 60/176,993
21 <151> PRIOR FILING DATE: 2000-01-19
23 <160> NUMBER OF SEQ ID NOS: 70
25 <170> SOFTWARE: PatentIn version 3.1
27 <210> SEQ ID NO: 1
28 <211> LENGTH: 1065
29 <212> TYPE: DNA
30 <213> ORGANISM: Human
32 <400> SEQUENCE: 1
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35 cgccagcccc agccgcatca tctcccgcaa ccgcccgcgc cgccgcagcc acctgcaact 120
37 ttgcaggcga gagagcatcc cgtctacccg cctgagctgt ccctcctgga cagcaccgac 180
39 ccacgcgcct ggctggctcc cactttgcag ggcactctga cggcacgcgc cgcccagtat 240
41 ttgctacatt ccccgagct ggtgctca gaggccgctg cgcccggga cgaggtggac 300
43 ggccggggg agctggttaag gaggagcagc ggcggtgcca gcagcagcaa gagccccggg 360
45 ccggtgaaag tgcgggaaca gctgtgcaag ctgaaaggcg ggtggtggt agacgagctg 420
47 ggctgcagcc gccaacgggc cccttccagc aaacagggtga atggggtgca gaagcagaga 480
49 cggctagcag ccaacgccag ggagcggcgc aggatgcatg ggctgaacca cgccttcgac 540
51 cagctgcgca atgttatccc gtcgttcaac aacgacaaga agctgtccaa atatgagacc 600
53 ctgcagatgg cccaaatcta catcaacgcc ttgtccgagc tgctacaaac gccagcgga 660
55 ggggaacagc caccgcccgc tccagcctcc tgcaaaagcg accaccacca ccttcgcacc 720
57 gcggcctcct atgaaggggg gcgaggcaac gcgaccgag ctggggctca gcaggcttcc 780
59 ggaggagacc agcggccgac cccgcccggg agttgcccga ctcgcttctc agcccagct 840
61 tctgcgggag ggtactcggg gcagctggag gctctgcact tctcgacttt cgaggacagc 900
63 gccctgacag cgatgatggc gcaaaaagaat ttgtctcctt ctctccccgg gagcatcttg 960
65 cagccagtgc aggagaaaaa cagcaaaact tcgcctcggg cccacagaag cgacggggaa 1020
67 ttttcccccc attcccatca cagtgactcg gatgaggcaa gtttag 1065
70 <210> SEQ ID NO: 2
71 <211> LENGTH: 354
72 <212> TYPE: PRT
73 <213> ORGANISM: Human

P.6

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75 <400> SEQUENCE: 2

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77 Met Ser Arg Leu Leu His Ala Glu Glu Trp Ala Glu Val Lys Glu Leu
78 1 5 10 15
81 Gly Asp His His Arg Gln Pro Gln Pro His His Leu Pro Gln Pro Pro
82 20 25 30
85 Pro Pro Pro Gln Pro Pro Ala Thr Leu Gln Ala Arg Glu His Pro Val
86 35 40 45
89 Tyr Pro Pro Glu Leu Ser Leu Asp Ser Thr Asp Pro Arg Ala Trp
90 50 55 60
93 Leu Ala Pro Thr Leu Gln Gly Ile Cys Thr Ala Arg Ala Ala Gln Tyr
94 65 70 75 80
97 Leu Leu His Ser Pro Glu Leu Gly Ala Ser Glu Ala Ala Ala Pro Arg
98 85 90 95
101 Asp Glu Val Asp Gly Arg Gly Glu Leu Val Arg Arg Ser Ser Gly Gly
102 100 105 110
105 Ala Ser Ser Ser Lys Ser Pro Gly Pro Val Lys Val Arg Glu Gln Leu
106 115 120 125
109 Cys Lys Leu Lys Gly Gly Val Val Val Asp Glu Leu Gly Cys Ser Arg
110 130 135 140
113 Gln Arg Ala Pro Ser Ser Lys Gln Val Asn Gly Val Gln Lys Gln Arg
114 145 150 155 160
117 Arg Leu Ala Ala Asn Ala Arg Glu Arg Arg Arg Met His Gly Leu Asn
118 165 170 175
121 His Ala Phe Asp Gln Leu Arg Asn Val Ile Pro Ser Phe Asn Asn Asp
122 180 185 190
125 Lys Lys Leu Ser Lys Tyr Glu Thr Leu Gln Met Ala Gln Ile Tyr Ile
126 195 200 205
129 Asn Ala Leu Ser Glu Leu Leu Gln Thr Pro Ser Gly Gly Glu Gln Pro
130 210 215 220
133 Pro Pro Pro Pro Ala Ser Cys Lys Ser Asp His His His Leu Arg Thr
134 225 230 235 240
137 Ala Ala Ser Tyr Glu Gly Gly Ala Gly Asn Ala Thr Ala Ala Gly Ala
138 245 250 255
141 Gln Gln Ala Ser Gly Gly Ser Gln Arg Pro Thr Pro Pro Gly Ser Cys
142 260 265 270
145 Arg Thr Arg Phe Ser Ala Pro Ala Ser Ala Gly Gly Tyr Ser Val Gln
146 275 280 285
149 Leu Asp Ala Leu His Phe Ser Thr Phe Glu Asp Ser Ala Leu Thr Ala
150 290 295 300
153 Met Met Ala Gln Lys Asn Leu Ser Pro Ser Leu Pro Gly Ser Ile Leu
154 305 310 315 320
157 Gln Pro Val Gln Glu Asn Ser Lys Thr Ser Pro Arg Ser His Arg
158 325 330 335
161 Ser Asp Gly Glu Phe Ser Pro His Ser His Tyr Ser Asp Ser Asp Glu
162 340 345 350
165 Ala Ser
169 <210> SEQ ID NO: 3
170 <211> LENGTH: 420
171 <212> TYPE: DNA

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177 gcggggacat tcccggacac acaccggagc agcagctgcg ccgcgacaca tctggagccg      120
179 cgtaggatgt tcgtcaaadc tgagactctg gagttgaagg aggaagagga ggtactgatg      180
181 ctgctgggct cggtctcccc ggctcggcg accctgaccc cgatgtcctc cagcgcggac      240
183 gaggaggagg acgaggagct gcgccggccg ggctccgcgc gtgggcagcg tggagcggaa      300
185 gccgggcagg gggcgcagg cagtcggcg tcgggtgcct ggggttgccg gacagggcgg      360
187 ctgctatgca ctgtgcacga gtgctagcgt gtgccgtcgc gctcacgggc cgtctgcaga      420
190 <210> SEQ ID NO: 4
191 <211> LENGTH: 645
192 <212> TYPE: DNA
193 <213> ORGANISM: MOUSE
195 <400> SEQUENCE: 4
196 atggcgctc atcccttgga tgcgtcacc atccaagtgt cccagagac acaacaacct      60
198 tttcccgag cctcggacca cgaagtgtc agttccaatt ccacccacc tagccccact      120
200 ctcataccta gggactgtc cgaagcagaa gtgggtgact gccgaggagac ctcgaggag      180
202 ctccgcgcc gacgcggagg gcgcaacagg cccaagagcg agttggcact cagcaaacag      240
204 cgaagaagcc ggcgcaagaa ggccaatgat cgggagcgca atcgcatgca caacctcaac      300
206 tcggcgctgg atgcgctgcg cgggtgtcctg cccaccttcc cggatgacgc caaacttaca      360
208 aagatcgaga cctgcgctt cgcccaacaac tacatctggg cactgactca gacgtgctgc      420
210 atagcggacc acagcttcta tggcccggag cccctgtgct cctgtggaga gctggggagc      480
212 cccggagggtg gctccaacgg ggactggggc tctatctact cccagctctc ccaagcgggt      540
214 aacctgagcc ccacggcctc attggaggaa ttccctggcc tgcagggtgcc cagctcccca      600
216 tcctatctgc tcccgggagc actggtgttc tcagacttct tgtga                      645
219 <210> SEQ ID NO: 5
220 <211> LENGTH: 214
221 <212> TYPE: PRT
222 <213> ORGANISM: MOUSE
224 <400> SEQUENCE: 5
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227 1 5 10 15
230 Thr Gln Gln Pro Phe Pro Gly Ala Ser Asp His Glu Val Leu Ser Ser
231 20 25 30
234 Asn Ser Thr Pro Pro Ser Pro Thr Leu Ile Pro Arg Asp Cys Ser Glu
235 35 40 45
238 Ala Glu Val Gly Asp Cys Arg Gly Thr Ser Arg Lys Leu Arg Ala Arg
239 50 55 60
242 Arg Gly Gly Arg Asn Arg Pro Lys Ser Glu Leu Ala Leu Ser Lys Gln
243 65 70 75 80
246 Arg Arg Ser Arg Arg Lys Lys Ala Asn Asp Arg Glu Arg Asn Arg Met
247 85 90 95
250 His Asn Leu Asn Ser Ala Leu Asp Ala Leu Arg Gly Val Leu Pro Thr
251 100 105 110
254 Phe Pro Asp Asp Ala Lys Leu Thr Lys Ile Glu Thr Leu Arg Phe Ala
255 115 120 125
258 His Asn Tyr Ile Trp Ala Leu Thr Gln Thr Leu Arg Ile Ala Asp His
259 130 135 140
262 Ser Phe Tyr Gly Pro Glu Pro Pro Val Pro Cys Gly Glu Leu Gly Ser

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263 145                      150                      155                      160
266 Pro Gly Gly Gly Ser Asn Gly Asp Trp Gly Ser Ile Tyr Ser Pro Val
267                      165                      170                      175
270 Ser Gln Ala Gly Asn Leu Ser Pro Thr Ala Ser Leu Glu Glu Phe Pro
271                      180                      185                      190
274 Gly Leu Gln Val Pro Ser Ser Pro Ser Tyr Leu Leu Pro Gly Ala Leu
275                      195                      200                      205
278 Val Phe Ser Asp Phe Leu
279      210
282 <210> SEQ ID NO: 6
283 <211> LENGTH: 1412
284 <212> TYPE: DNA
285 <213> ORGANISM: MOUSE
287 <400> SEQUENCE: 6
288 cgtgctcggg tccgggctgc ggggacattc cgggacacac accggagcag cagctgcgcc      60
290 gcgacacatc tggagccgcg taggatgttc gtcaaactct agactctgga gttgaaggag      120
292 gaagaggagg tactgatgct gctgggctcg gcttcccccg cctcggcgac cctgaccccg      180
294 atgtcctcca gcgcggacga ggaggaggac gaggagctgc gccggccggg ctccgcgcgt      240
296 gggcagcgtg gagcggaagc cgggcagggg gtgcagggca gtccggcgtc gggtgccggg      300
298 ggttgccggc cagggcggct gctgggcctg atgcacgagt gcaagcgtcg cccgtcgcgc      360
300 tcacgggccc tctcccagag tgccaagacg gcggagacgg tgcagcgcat caagaagacc      420
302 cgcaggctca aggccaacaa ccgcgagcgc aaccgcatgc acaacctaaa cgccgcgctg      480
304 gacgcgctgc gcgaggtgct gcccaccttc cccgaggatg ccaagctcac gaagatcgag      540
306 acgtgcgctc tcgcccacaa ttacatctgg gcgctcaccg agactctgcg cctggcggac      600
308 cactgcgccg gcgccggtgg cctccagggg gcgctcttca cggaggcggg gctcctgagc      660
310 ccgggagctg cgctcggcgc cagcggggag agcccttctc caccttctct ctggagctgc      720
312 accaacagcc cggcgctcat ctccaactcc acgtcccatc acagctgcac tttatcgccc      780
314 gctagccccg ggtcagacgt ggactactgg cagccccac ctccggagaa gcatcgttat      840
316 gcgcctcacc tgcccctcgc cagggactgt atctagagct gcgggtctcc ctctctcgtc      900
318 ctctaccgag cctcttctcc atccttctcc cgcccctcac cctccacgcc ccggactcca      960
320 cttcacagag cagaggtggc ccttgcaatc cctcggcgcg ctggtgcatt cgggggtgga      1020
322 gaccagctct ggtttattga agatgtgagg atttatggtc aaagaggact atggcgtgtg      1080
324 ggagtggggg ctggcgtggg gaacctcgta agactgtaaa agacactgag aaaaagtacc      1140
326 ataactaacg agtgtgcaga gcagactgac gctcctcccc tctctcagag ctgctggagg      1200
328 agaactccgg gcaggcagtt cgtgtgaatc tctcagaggg aatgcaactg gtccctgtga      1260
330 tcttttcacc ttcgtttcta catagagatg ttaatgtcag tcgaaagaaa tgtattttag      1320
332 catctgaatg aattttactg taataatatt atccacacat ttgcaatggc tggcatctgc      1380
334 tctattccca ttgctgtctg caggctgtgg ga                                     1412
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338 <211> LENGTH: 263
339 <212> TYPE: PRT
340 <213> ORGANISM: MOUSE
342 <400> SEQUENCE: 7
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348 Leu Met Leu Leu Gly Ser Ala Ser Pro Ala Ser Ala Thr Leu Thr Pro
349      20                      25                      30
352 Met Ser Ser Ser Ala Asp Glu Glu Glu Asp Glu Glu Leu Arg Arg Pro
353      35                      40                      45

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356 Gly Ser Ala Arg Gly Gln Arg Gly Ala Glu Ala Gly Gln Gly Val Gln
357      50                      55                      60
360 Gly Ser Pro Ala Ser Gly Ala Gly Gly Cys Arg Pro Gly Arg Leu Leu
361 65                      70                      75                      80
364 Gly Leu Met His Glu Cys Lys Arg Arg Pro Ser Arg Ser Arg Ala Val
365                      85                      90                      95
368 Ser Arg Gly Ala Lys Thr Ala Glu Thr Val Gln Arg Ile Lys Lys Thr
369                      100                     105                     110
372 Arg Arg Leu Lys Ala Asn Asn Arg Glu Arg Asn Arg Met His Asn Leu
373                      115                     120                     125
376 Asn Ala Ala Leu Asp Ala Leu Arg Glu Val Leu Pro Thr Phe Pro Glu
377                      130                     135                     140
380 Asp Ala Lys Leu Thr Lys Ile Glu Thr Leu Arg Phe Ala His Asn Tyr
381 145                      150                      155                      160
384 Ile Trp Ala Leu Thr Glu Thr Leu Arg Leu Ala Asp His Cys Ala Gly
385                      165                      170                      175
388 Ala Gly Gly Leu Gln Gly Ala Leu Phe Thr Glu Ala Val Leu Leu Ser
389                      180                      185                      190
392 Pro Gly Ala Ala Leu Gly Ala Ser Gly Asp Ser Pro Ser Pro Pro Ser
393                      195                     200                     205
396 Ser Trp Ser Cys Thr Asn Ser Pro Ala Ser Ser Ser Asn Ser Thr Ser
397                      210                     215                     220
400 Pro Tyr Ser Cys Thr Leu Ser Pro Ala Ser Pro Gly Ser Asp Val Asp
401 225                      230                      235                      240
404 Tyr Trp Gln Pro Pro Pro Glu Lys His Arg Tyr Ala Pro His Leu
405                      245                      250                      255
408 Pro Leu Ala Arg Asp Cys Ile
409                      260

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412 <210> SEQ ID NO: 8

413 <211> LENGTH: 1957

414 <212> TYPE: DNA

415 <213> ORGANISM: MOUSE

417 <400> SEQUENCE: 8

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422 aagaaccatg ttaacactac cgtttgacga gtctgtcgta atgcccgaaat cccagatgtg      180
424 cagaaaagttt gctagacaat gtgaggacca gaaacaaatt aagaaaccag agagctttcc      240
426 aaaacaagtt gtccttcgag gaaagagcat taaaagggcc cctggagaag aaaccgagaa      300
428 agaagaggag gaagaagaca gagaggaaga agatgagaat ggcttgtcca gaaggagggg      360
430 gtcaggaaaa aaaaagacca ccaaactacg actggaaagg gtcaagttca ggagacagga      420
432 agctaattgcg cgcgagagga accggatgca cggcctcaat gatgctctgg acaatttgcg      480
434 aaaagtggtc ccctgttact ctaaaaccca aaaactgtcc aaaatagaaa ctttacgact      540
436 ggccaaaaat tacatctggg cactttctga aattctgagg attggcaaga gaccggatct      600
438 gctcacgttc gtccaaaact tatgcaaagg tctttcccag ccaactacaa acttggtggc      660
440 aggtctgctta cagctcaacg ccgaagttt cctgatgggt cagggtgggg aggtgcccac      720
442 ccacacaagg tcaccctact ccacattcta cccaccctac cacagccctg agctggccac      780
444 tccccaggg catgggactc ttgataattc caagtccatg aaaccctaca attactgcag      840
446 tgcataatgaa tccttctatg aaagtacctc ccctgagtgt gccagccctc agtttgaagg      900
448 tcccttaagt cctcccccaa ttaactataa tgggatattt tccctgaagc aagaagaaac      960

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RAW SEQUENCE LISTING ERROR SUMMARY DATE: 01/28/2003
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:13; N Pos. 115
Seq#:16; N Pos. 203,217
Seq#:57; N Pos. 1497,1504,1526,1564
Seq#:59; N Pos. 147

Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:1; Line(s) 9